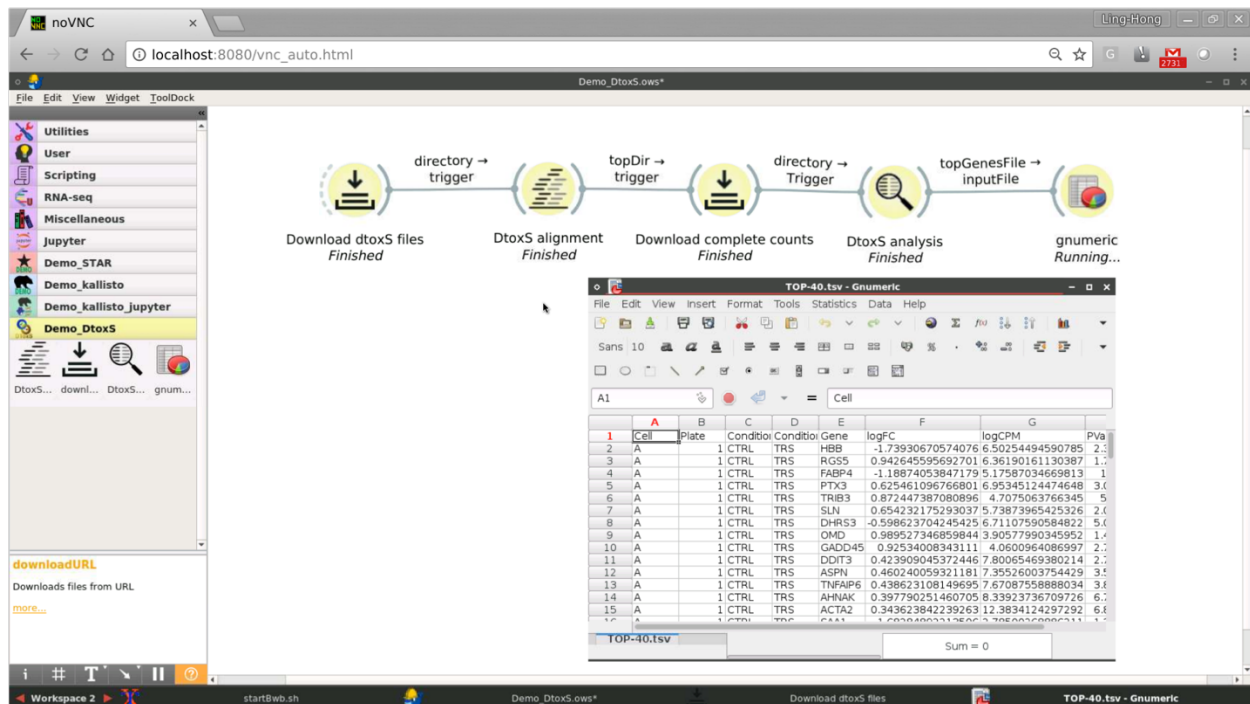
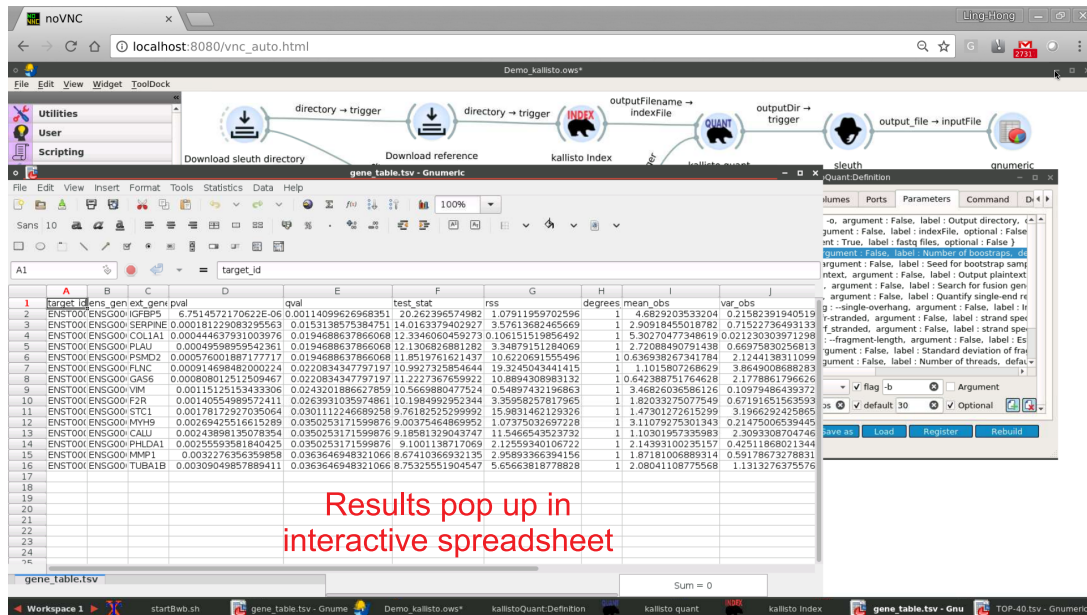


**Supplemental Figure S1.** Related to Figure 1 and the STAR Methods. Screenshot of DToxS workflow demo: The DToxS RNA-seq workflow is implemented as a demonstration of the Bwb. The connected workflow consists of five connected widgets, and processes RNA-seq fastq files to obtain a list of differentially expressed genes. This list is displayed using the gnumeric spreadsheet.



**Supplemental Figure S2.** Related to Figure 2 and the STAR Methods. Graphical output of kallisto-sleuth workflow. Sleuth has its output linked to the trigger of the gnumeric spreadsheet. When sleuth is finished processing it sends the output to the trigger which prompts the gnumeric application to read the output CSV file and display the results. The popup window is a normal gnumeric window enabling the user to interact with the process to visualize the data while saving results to a host file.



**Supplemental Figure S3.** Related to the STAR Methods. STAR/DESeq2 RNA-seq workflow on remote servers: The Bwb workflow consists of nine widgets and implements a RNA-seq differential gene expression pipeline. This is very similar in structure to the kallisto-sleuth pipeline. However, the STAR aligner requires more RAM (32 GB) than available on our laptop and the screenshot image depicts a browser connecting to the Bwb application running on a remote local firewalled server. The connection is established using SSH tunneling. The gnumeric application displays a popup window (lower right window) to view the final results and works identically when run remotely. The scrollable lower left window pops up upon clicking the STAR align widget. It shows some of the many parameters that the STAR aligner uses, that are carried along with the Bwb workflow that are easily customized.

The screenshot displays a noVNC browser interface connected to a remote server. The main window shows the 'Demo\_STAR' workflow, a sequence of nine widgets: 'Download STAR tutorial setup files', 'Download release-91 GRCh38 files', 'Star index', 'Star Align', 'Star to DESeq2', 'DESeq2', 'topGenesFile', and 'gnumeric'. The 'Star Align' widget is currently active, showing a configuration panel with 'Required entries' (outStd, outReadsUnmapped, outMultimapOrder, outSAMtype, outSAMmode, outSAMstrandField, outSAMattributes, outSAMunmapped, outSAMorder, outSAMprimaryFlag, outSAMreadID) and 'Optional entries' (Log, Old\_2.4, SAM, Full, Enter parameter, Standard, Paired, OneBestScore, Standard). The 'Console' tab shows the workflow progress. A 'Star Align' popup window is open, displaying a table of results. The table has columns: Gene, baseMean, log2FoldChange, lfcSE, stat, and pval. The results show a list of genes with their corresponding values.

| Gene | baseMean         | log2FoldChange     | lfcSE              | stat              | pval    |
|------|------------------|--------------------|--------------------|-------------------|---------|
| 1    | 529.310248454029 | 1.31800306038746   | 0.102544383550771  | 12.8530009616266  | 6.8e-06 |
| 2    | 97.8484576838374 | 2.26218896254328   | 0.199845279132399  | 11.3197017831208  | 1.1e-05 |
| 3    | 106.402901094778 | -1.99689355711945  | 0.185118812553968  | -10.7870914337099 | 3.3e-05 |
| 4    | 37.8642336937058 | 2.94809127538995   | 0.349796040113684  | 8.4280293008229   | 3.3e-05 |
| 5    | 71.995933713024  | 1.72568685125944   | 0.209416491637661  | 8.24045345122712  | 1.1e-05 |
| 6    | 38.802987789821  | 2.37664899870641   | 0.302640188002789  | 7.85305155402726  | 4.4e-05 |
| 7    | 40.265179921758  | -2.33188944604097  | 0.29796046550364   | -7.82617068806786 | 5.5e-05 |
| 8    | 32.9793185825887 | 2.38082546196769   | 0.325850785277331  | 7.30648987063626  | 2.2e-05 |
| 9    | 153.314680324944 | 1.14162631347756   | 0.16154498724486   | 7.06692502780763  | 1.1e-05 |
| 10   | 24.6683547824314 | 3.00694982413176   | 0.424463756920288  | 7.08411442698616  | 1.1e-05 |
| 11   | 43.1896631148596 | 1.95542070849786   | 0.276202992478536  | 7.07965069802717  | 1.1e-05 |
| 12   | 240.841573681108 | -0.888478802525573 | 0.129377152669897  | -6.86735473915174 | 6.8e-06 |
| 13   | 999.108758687274 | -0.578849118436642 | 0.0844332223160988 | -6.85570327127351 | 6.8e-06 |
| 14   | 31.4601307591763 | 2.20089402070229   | 0.326423768156096  | 6.74244413369378  | 1.1e-05 |
| 15   | 32.4631572860181 | 2.10978401047877   | 0.315718972345405  | 6.68247459063227  | 2.2e-05 |
| 16   | 35.1276993822045 | -1.9667110140444   | 0.295165880654097  | -6.66307030367503 | 2.2e-05 |
| 17   | 109.575883556264 | -1.12267814298748  | 0.168656660501875  | -6.65658942639264 | 2.2e-05 |
| 18   | 61.737694766984  | -1.40673480508481  | 0.218692677216086  | -6.43247329079447 | 1.1e-05 |
| 19   | 175.765485802794 | -0.883572204505092 | 0.14485376592266   | -6.09975307771321 | 1.1e-05 |

**Supplemental Figure S4.** Related to Figure 1, Figure 2 and the STAR Methods. Widget panels: each widget has two tabbed panels. Double-clicking on the kallisto-quant widget in the kallisto-sleuth pipeline launches a data entry panel with a series of tabs. The numerous optional parameters that control the way that kallisto performs its quantifications are exposed by clicking on the 'optional' tab. Right-clicking the kallisto-quant widget, and choosing edit brings up the widget definition panel. This reveals the settings that define the widget itself. The blue highlighted selection in the parameters tab of the kallisto:definition window shows the parameters defining the number of bootstrap options. The user can enter new values into the definition:window to change the default number of bootstraps, for example. Finally, the black background window on the left is the console of the kallisto index. It displays the messages being printed by the widget as it processes the data. The data remains in the window for review until cleared.

